Nucleotide and amino acid sequences (see SEQ ID NO: 1 and 2) of a primate, e.g., human, IL-7Rα; predicted signal cleavage site indicated.

```
ctctctctct atctctctca ga atg aca att cta ggt aca act ttt ggc atg  52
                         Met Thr Ile Leu Gly Thr Thr Phe Gly Met
                         -20                 -15

gtt ttt tct tta ctt caa gtc gtt tct gga gaa agt ggc tat gct caa  100
Val Phe Ser Leu Leu Gln Val Val Ser Gly Glu Ser Gly Tyr Ala Gln
-10                  -5              -1   1               5

aat gga gac ttg gaa gat gca gaa ctg gat gac tac tca ttc tca tgc  148
Asn Gly Asp Leu Glu Asp Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys
             10                  15                  20

tat agc cag ttg gaa gtg aat gga tcg cag cat tca ctg acc tgt gct  196
Tyr Ser Gln Leu Glu Val Asn Gly Ser Gln His Ser Leu Thr Cys Ala
         25                  30                  35

ttt gag gac cca gat gtc aac acc acc aat ctg gaa ttt gaa ata tgt  244
Phe Glu Asp Pro Asp Val Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys
     40                  45                  50

ggg gcc ctc gtg gag gta aag tgc ctg aat ttc agg aaa cta caa gag  292
Gly Ala Leu Val Glu Val Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu
 55                  60                  65                  70
```

FIG. 1A

```
ata tat ttc atc gag aca aag aaa ttc tta ctg att gga aag agc aat   340
Ile Tyr Phe Ile Glu Thr Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn
                75                  80                  85

ata tgt gtg aag gtt gga gaa aag agt cta acc tgc aaa aaa ata gac   388
Ile Cys Val Lys Val Gly Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp
            90                  95                 100

cta acc act ata gtt aaa cct gag gct cct ttt gac ctg agt gtc atc   436
Leu Thr Thr Ile Val Lys Pro Glu Ala Pro Phe Asp Leu Ser Val Ile
        105                 110                 115

tat cgg gaa gga gcc aat gac ttt gtg gtg aca ttt aat aca tca cac   484
Tyr Arg Glu Gly Ala Asn Asp Phe Val Val Thr Phe Asn Thr Ser His
    120                 125                 130

ttg caa aag aag tat gta aaa gtt tta atg cat gat gta gct tac cgc   532
Leu Gln Lys Lys Tyr Val Lys Val Leu Met His Asp Val Ala Tyr Arg
135                 140                 145                 150

cag gaa aag gat gaa aac aaa tgg acg cat gtg aat tta tcc agc aca   580
Gln Glu Lys Asp Glu Asn Lys Trp Thr His Val Asn Leu Ser Ser Thr
                155                 160                 165
```

FIG. 1B

```
aag ctg aca ctc ctg cag aga aag ctc caa ccg gca gca atg tat gag   628
Lys Leu Thr Leu Leu Gln Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu
            170                 175                 180

att aaa gtt cga tcc atc cct gat cac tat ttt aaa ggc ttc tgg agt   676
Ile Lys Val Arg Ser Ile Pro Asp His Tyr Phe Lys Gly Phe Trp Ser
        185                 190                 195

gaa tgg agt cca agt tat tac ttc aga act cca gag atc aat aat agc   724
Glu Trp Ser Pro Ser Tyr Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser
    200                 205                 210

tca ggg gag atg gat cct atc tta cta acc atc agc att ttg agt ttt   772
Ser Gly Glu Met Asp Pro Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe
215                 220                 225                 230

ttc tct gtc gct ctg ttg gtc atc ttg gcc tgt gtg tta tgg aaa aaa   820
Phe Ser Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys
                235                 240                 245

agg att aag cct atc gta tgg ccc agt ctc ccc gat cat aag aag act   868
Arg Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr
            250                 255                 260

ctg gaa cat ctt tgt aag aaa cca aga aaa aat tta aat gtg agt ttc   916
Leu Glu His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe
        265                 270                 275
```

FIG. 1C

```
aat cct gaa agt ttc ctg gac tgc cag att cat agg gtg gat gac att   964
Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile
    280                 285                 290

caa gct aga gat gaa gtg gaa ggt ttt ctg caa gat acg ttt cct cag  1012
Gln Ala Arg Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln
295                 300                 305                 310

caa cta gaa gaa tct gag aag cag agg ctt gga ggg gat gtg cag agc  1060
Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser
                315                 320                 325

ccc aac tgc cca tct gag gat gta gtc gtc act cca gaa agc ttt gga  1108
Pro Asn Cys Pro Ser Glu Asp Val Val Val Thr Pro Glu Ser Phe Gly
            330                 335                 340

aga gat tca tcc ctc aca tgc ctg gct ggg aat gtc agt gca tgt gac  1156
Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp
        345                 350                 355

gcc cct att ctc tcc tct tcc agg tcc cta gac tgc agg gag agt ggc  1204
Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly
    360                 365                 370

aag aat ggg cct cat gtg tac cag gac ctc ctg ctt agc ctt ggg act  1252
Lys Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr
375                 380                 385                 390
```

FIG. 1D

```
aca aac agc acg ctg ccc cct cca ttt tct ctc caa tct gga atc ctg    1300
Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu
                395                 400                 405

aca ttg aac cca gtt gct cag ggt cag ccc att ctt act tcc ctg gga    1348
Thr Leu Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly
            410                 415                 420

tca aat caa gaa gaa gca tat gtc acc atg tcc agc ttc tac caa aac    1396
Ser Asn Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn
        425                 430                 435

cag tgaagtgtaa gaaacccaga ctgaacttac cgtgagcgac aaagatgatt         1449
Gln

taaaagggaa gtctagagtt cctagtctcc ctcacagcac agagaagaca aaattagcaa 1509

aaccccacta cacagtctgc aagattctga aacattgctt tgaccactct tcctgagttc 1569

agtggcactc aacatgagtc aagagcatcc tgcttctacc atgtggattt ggtcacaagg 1629

tttaaggtga cccaatgatt cagctattt                                    1658
```

FIG. 1E

Nucleotide and amino acid sequences (see SEQ ID NO: 3 and 4) of a primate, e.g., human, Rδ2; predicted signal cleavage site indicated.

```
cggcacgagg gc atg ggg cgg ctg gtt ctg ctg tgg gga gct gcc gtc ttt 51
              Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe
                     -20                 -15                 -10

ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga   99
Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly
                -5              -1   1               5

gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca   147
Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr
         10                  15                  20

tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga   195
Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg
     25                  30                  35

ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag   243
Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln
 40                  45                  50                  55

gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac   291
Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp
                60                  65                  70
```

FIG. 2A

```
att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca   339
Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala
            75                  80                  85

agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg   387
Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val
        90                  95                  100

aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg   435
Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu
    105                 110                 115

tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac   483
Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp
120                 125                 130                 135

acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa   531
Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu
                140                 145                 150

ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct   579
Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala
            155                 160                 165

atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag   627
Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu
        170                 175                 180
```

FIG. 2B

```
gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca   675
Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr
    185                 190                 195

cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc   723
Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser
200                 205                 210                 215

ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa   771
Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys
                220                 225                 230

tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa   819
Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys
            235                 240                 245

tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag   867
Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu
        250                 255                 260

tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt   915
Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly
    265                 270                 275

gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc   963
Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala
280                 285                 290                 295
```

FIG. 2C

```
aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag    1011
Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu
                300                 305                 310

aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa    1059
Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln
            315                 320                 325

ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac    1107
Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp
        330                 335                 340

cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt           1155
Arg Ser Tyr Val Ala Leu
    345
```

FIG. 2D

caggatccac gttgacattt aaagacagag gggactgtcc cggggactcc acaccaccat 1215

ggatgggaag tctccacgcc aatgatggta ggactaggag actctgaaga cccagcctca 1275

ccgcctaatg cggccactgc cctgctaact ttcccccaca tgagtctctg tgttcaaagg 1335

cttgatggca gatgggagcc aattgctcca ggagatttac tcccagttcc ttttcgtgcc 1395

tgaacgttgt cacataaacc ccaaggcagc acgtccaaaa tgctgtaaaa ccatcttccc 1455

actctgtgag tccccagttc cgtccatgta cctgttccat agcattggat tctcggagga 1515

ttttttgtct gttttgagac tccaaaccac ctctacccct ac 1557

FIG. 2E

```
MFPFALLYVLSVSFRKIFILQLVGLVLTYD  30
FTNCDFEKIKAAYLSTISKDLITYMSGTKS  60
TEFNNTVSCSNRPHCLTEIQSLTFNPTAGC  90
ASLAKEMFAMKTKAALAIWCPGYSETQINA  120
TQAMKKRRKRKVTTNKCLEQVSQLQGLWRR  150
FNRPLLKQQ
```

FIG. 3A

```
1    agtgtgaaac tggggtggaa tgggtgtcca cgtatgttcc cttttgcctt
51   actatatgtt ctgtcagttt ctttcaggaa aatcttcatc ttacaacttg
101  tagggctggt gttaacttac gacttcacca actgtgactt tgagaagatt
151  aaagcagcct atctcagtac tatttctaaa gacctgatta catatatgag
201  tgggaccaaa agtaccgagt tcaacaacac cgtctcttgt agcaatcggc
251  cacattgcct tactgaaatc cagagcctaa ccttcaatcc caccgccggc
301  tgcgcgtcgc tcgccaaaga aatgttcgcc atgaaaacta aggctgcctt
351  agctatctgg tgcccaggct attcggaaac tcagataaat gctactcagg
401  caatgaagaa gaggagaaaa aggaaagtca caaccaataa atgtctggaa
451  caagtgtcac aattacaagg attgtggcgt cgcttcaatc gacccttact
501  gaaacaacag taaaccatct ttattatggt catatttcac agcaccaaaa
     ta
```

FIG. 3B

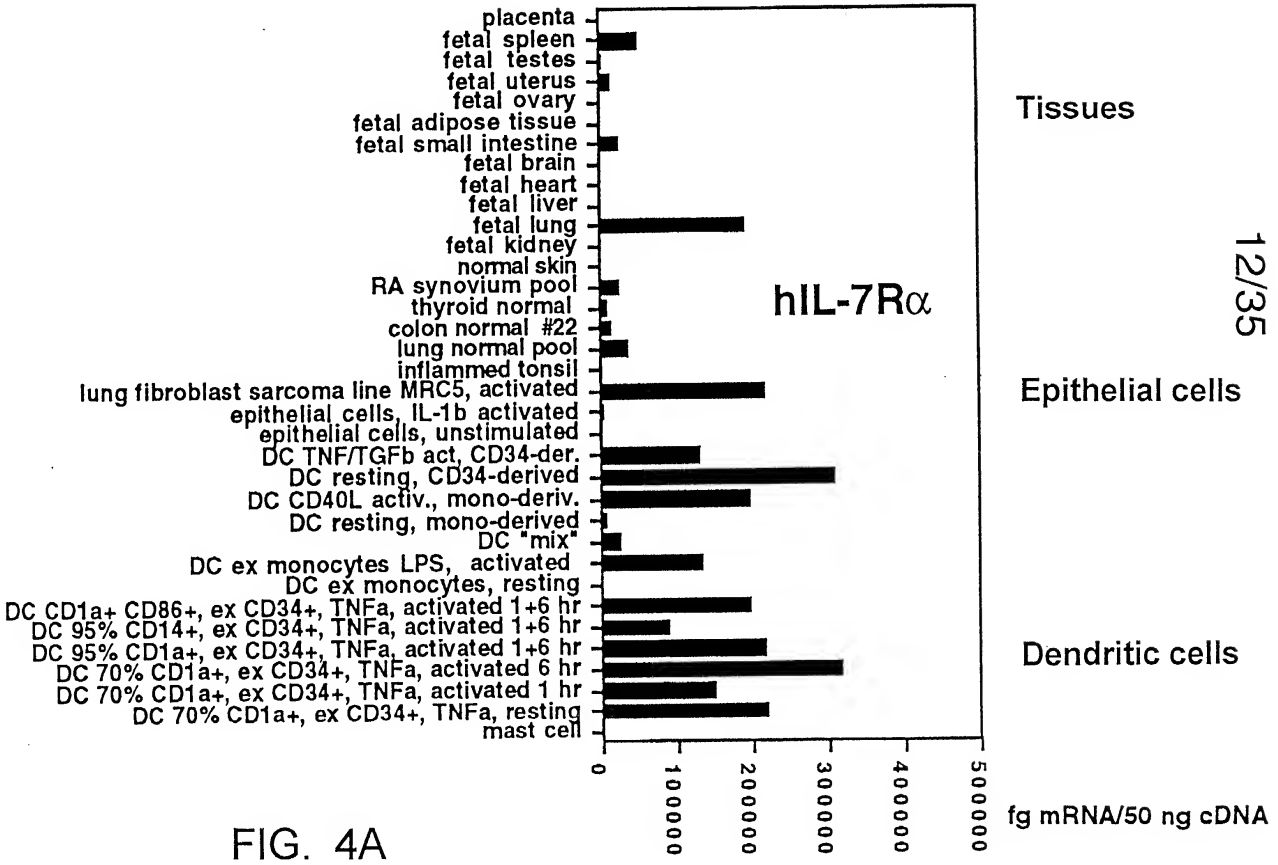

placenta
fetal spleen
fetal testes
fetal uterus
fetal ovary
fetal adipose tissue
fetal small intestine
fetal brain
fetal heart
fetal liver
fetal lung
fetal kidney
normal skin
RA synovium pool
thyroid normal
colon normal #22
lung normal pool
inflammed tonsil
lung fibroblast sarcoma line MRC5, activated
epithelial cells, IL-1b activated
epithelial cells, unstimulated
DC TNF/TGFb act, CD34-der.
DC resting, CD34-derived
DC CD40L activ., mono-deriv.
DC resting, mono-derived
DC "mix"
DC ex monocytes LPS, activated
DC ex monocytes, resting
DC CD1a+ CD86+, ex CD34+, TNFa, activated 1+6 hr
DC 95% CD14+, ex CD34+, TNFa, activated 1+6 hr
DC 95% CD1a+, ex CD34+, TNFa, activated 1+6 hr
DC 70% CD1a+, ex CD34+, TNFa, activated 6 hr
DC 70% CD1a+, ex CD34+, TNFa, activated 1 hr
DC 70% CD1a+, ex CD34+, TNFa, resting
mast cell
hIL-7Rα
Tissues
Epithelial cells
Dendritic cells
0
100000
200000
300000
400000
500000
fg mRNA/50 ng cDNA

FIG. 4A

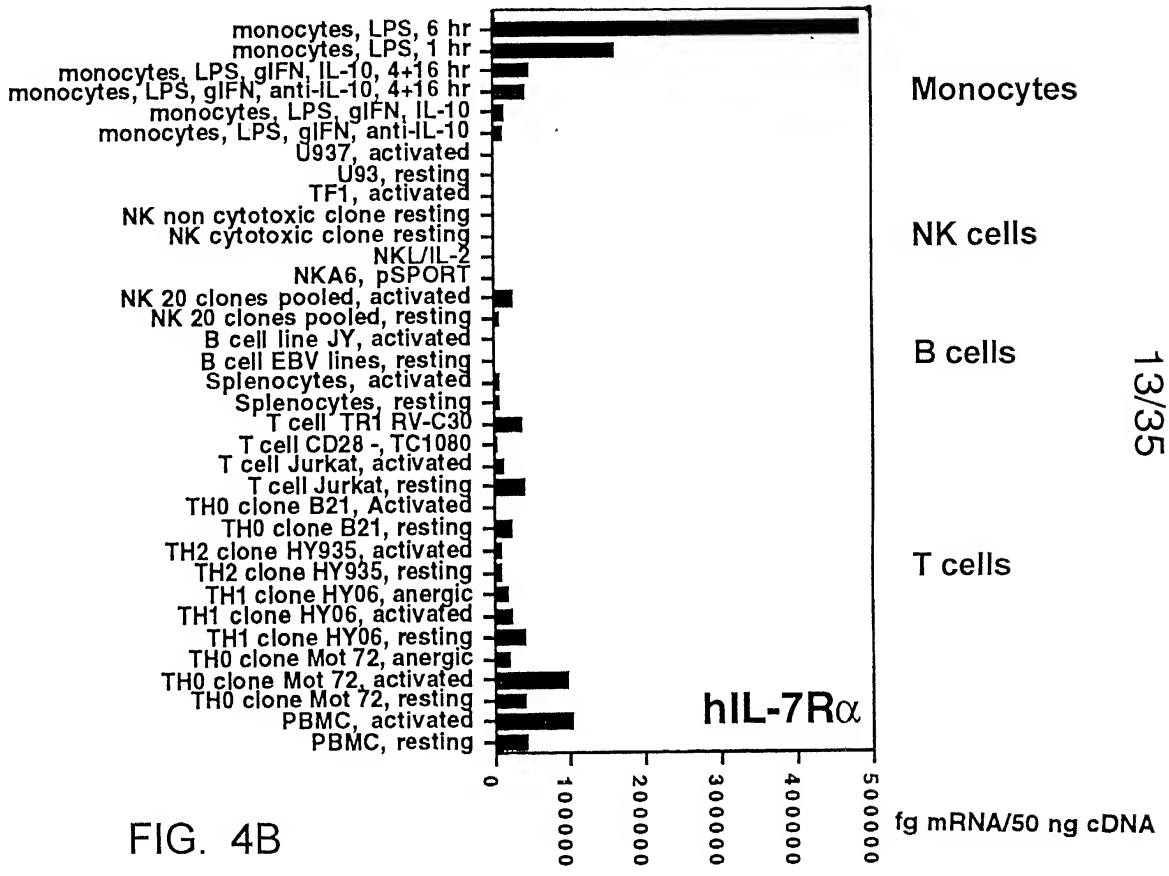

monocytes, LPS, 6 hr
monocytes, LPS, 1 hr
monocytes, LPS, gIFN, IL-10, 4+16 hr
monocytes, LPS, gIFN, anti-IL-10, 4+16 hr
monocytes, LPS, gIFN, IL-10
monocytes, LPS, gIFN, anti-IL-10
U937, activated
U93, resting
TF1, activated
NK non cytotoxic clone resting
NK cytotoxic clone resting
NKL/IL-2
NKA6, pSPORT
NK 20 clones pooled, activated
NK 20 clones pooled, resting
B cell line JY, activated
B cell EBV lines, resting
Splenocytes, activated
Splenocytes, resting
T cell TR1 RV-C30
T cell CD28 -, TC1080
T cell Jurkat, activated
T cell Jurkat, resting
TH0 clone B21, Activated
TH0 clone B21, resting
TH2 clone HY935, activated
TH2 clone HY935, resting
TH1 clone HY06, anergic
TH1 clone HY06, activated
TH1 clone HY06, resting
TH0 clone Mot 72, anergic
TH0 clone Mot 72, activated
TH0 clone Mot 72, resting
PBMC, activated
PBMC, resting
Monocytes
NK cells
B cells
T cells
hIL-7Rα
0
100000
200000
300000
400000
500000
fg mRNA/50 ng cDNA

FIG. 4B

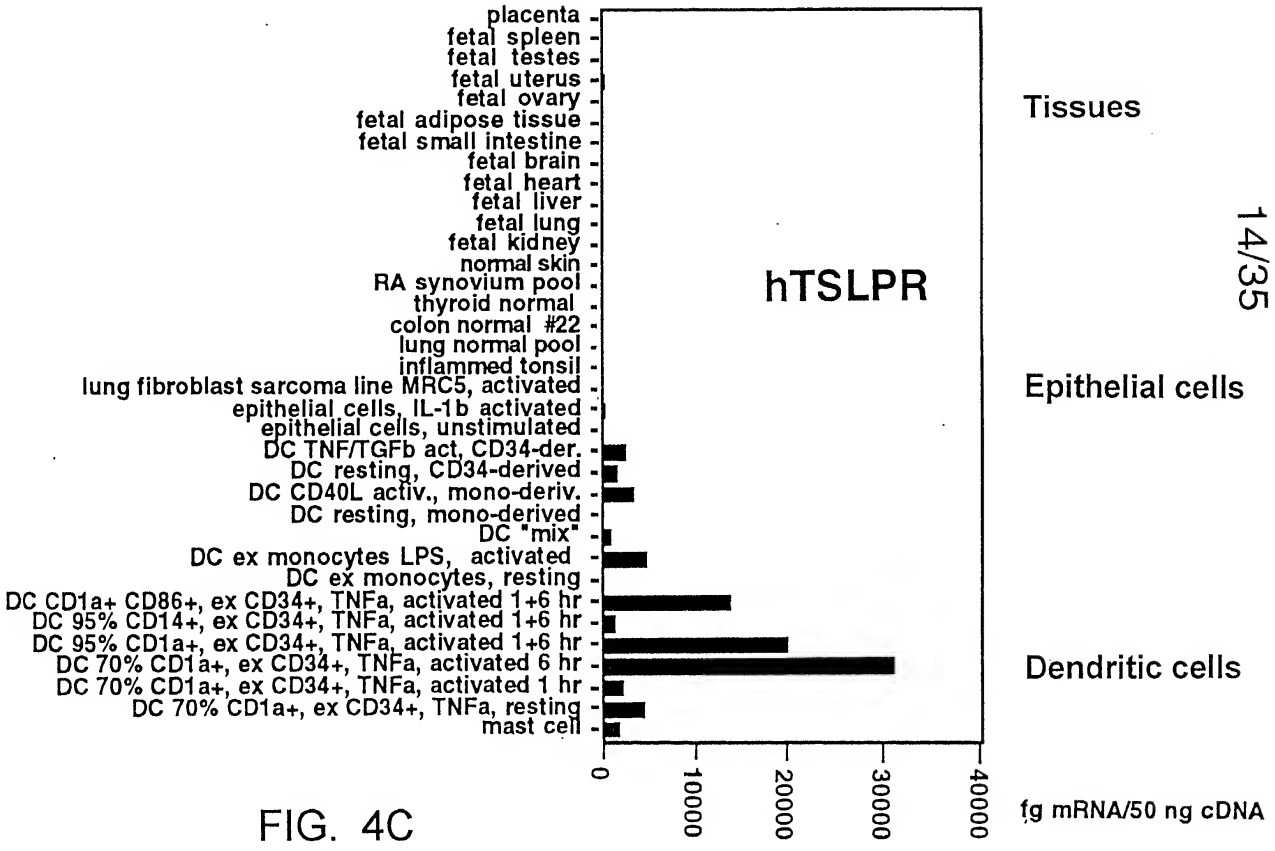

placenta
fetal spleen
fetal testes
fetal uterus
fetal ovary
fetal adipose tissue
fetal small intestine
fetal brain
fetal heart
fetal liver
fetal lung
fetal kidney
normal skin
RA synovium pool
thyroid normal
colon normal #22
lung normal pool
inflammed tonsil
lung fibroblast sarcoma line MRC5, activated
epithelial cells, IL-1b activated
epithelial cells, unstimulated
DC TNF/TGFb act, CD34-der.
DC resting, CD34-derived
DC CD40L activ., mono-deriv.
DC resting, mono-derived
DC "mix"
DC ex monocytes LPS, activated
DC ex monocytes, resting
DC CD1a+ CD86+, ex CD34+, TNFa, activated 1+6 hr
DC 95% CD14+, ex CD34+, TNFa, activated 1+6 hr
DC 95% CD1a+, ex CD34+, TNFa, activated 1+6 hr
DC 70% CD1a+, ex CD34+, TNFa, activated 6 hr
DC 70% CD1a+, ex CD34+, TNFa, activated 1 hr
DC 70% CD1a+, ex CD34+, TNFa, resting
mast cell
hTSLPR
Tissues
Epithelial cells
Dendritic cells
0
10000
20000
30000
40000
fg mRNA/50 ng cDNA

FIG. 4C

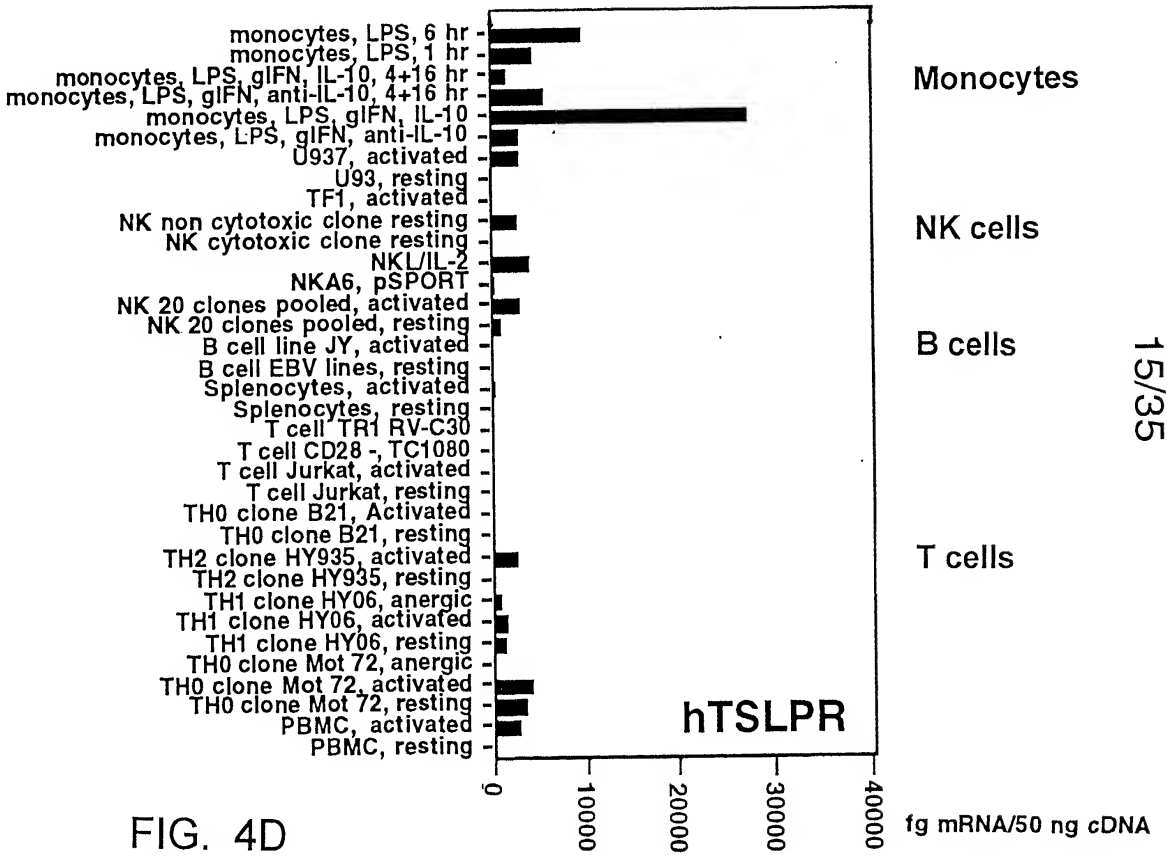

monocytes, LPS, 6 hr
monocytes, LPS, 1 hr
monocytes, LPS, gIFN, IL-10, 4+16 hr
monocytes, LPS, gIFN, anti-IL-10, 4+16 hr
monocytes, LPS, gIFN, IL-10
monocytes, LPS, gIFN, anti-IL-10
U937, activated
U93, resting
TF1, activated
NK non cytotoxic clone resting
NK cytotoxic clone resting
NKL/IL-2
NKA6, pSPORT
NK 20 clones pooled, activated
NK 20 clones pooled, resting
B cell line JY, activated
B cell EBV lines, resting
Splenocytes, activated
Splenocytes, resting
T cell TR1 RV-C30
T cell CD28 -, TC1080
T cell Jurkat, activated
T cell Jurkat, resting
TH0 clone B21, Activated
TH0 clone B21, resting
TH2 clone HY935, activated
TH2 clone HY935, resting
TH1 clone HY06, anergic
TH1 clone HY06, activated
TH1 clone HY06, resting
TH0 clone Mot 72, anergic
TH0 clone Mot 72, activated
TH0 clone Mot 72, resting
PBMC, activated
PBMC, resting
Monocytes
NK cells
B cells
T cells
hTSLPR
0
10000
20000
30000
40000
fg mRNA/50 ng cDNA

FIG. 4D

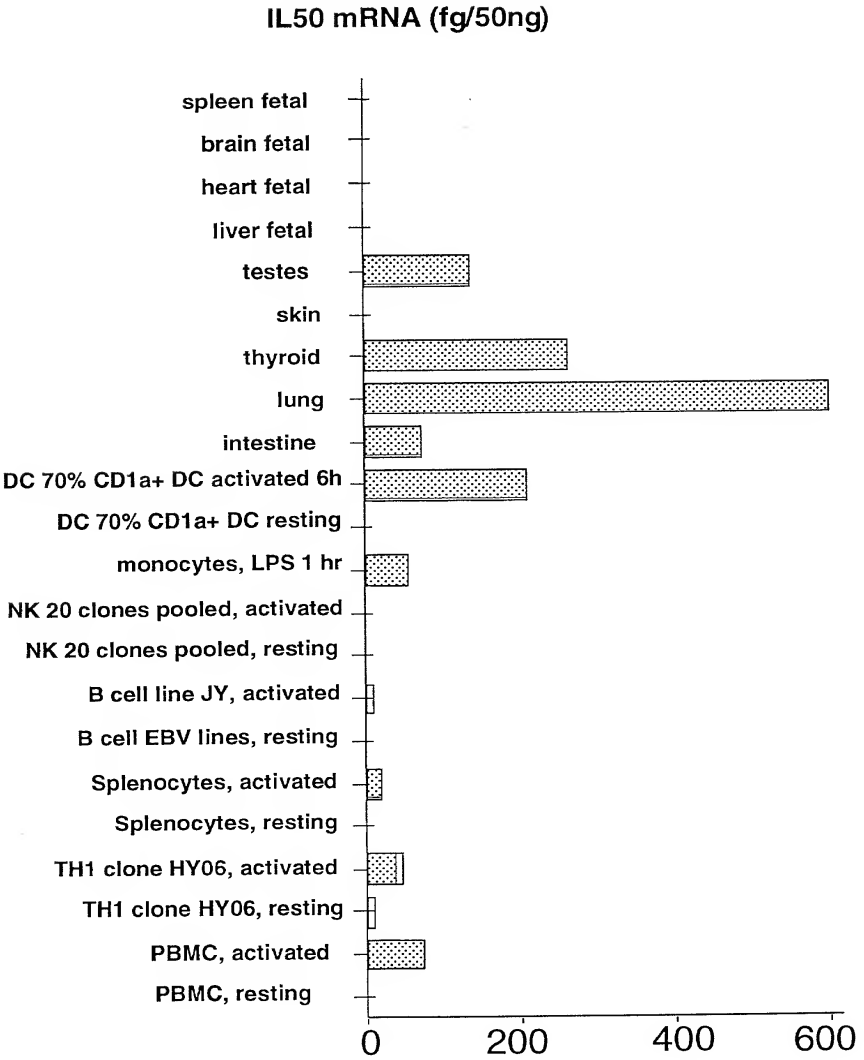

IL50 mRNA (fg/50ng)
spleen fetal
brain fetal
heart fetal
liver fetal
testes
skin
thyroid
lung
intestine
DC 70% CD1a+ DC activated 6h
DC 70% CD1a+ DC resting
monocytes, LPS 1 hr
NK 20 clones pooled, activated
NK 20 clones pooled, resting
B cell line JY, activated
B cell EBV lines, resting
Splenocytes, activated
Splenocytes, resting
TH1 clone HY06, activated
TH1 clone HY06, resting
PBMC, activated
PBMC, resting
0
200
400
600

FIG. 4E

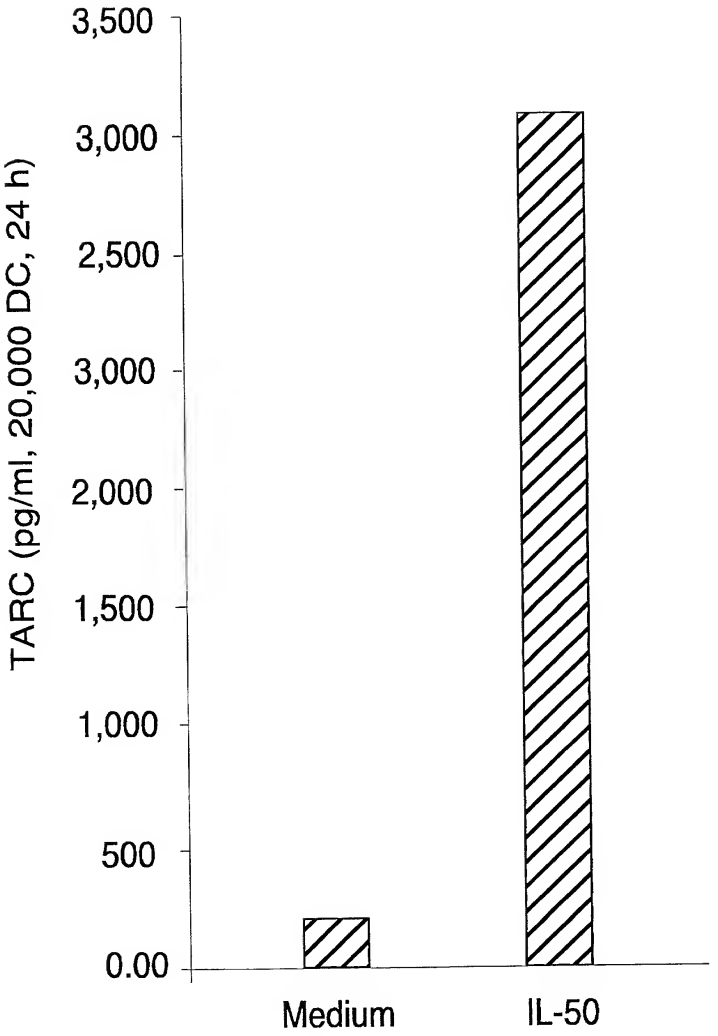

3,500
3,000
2,500
3,000
2,000
1,500
1,000
500
0.00
TARC (pg/ml, 20,000 DC, 24 h)
Medium
IL-50

FIG. 5

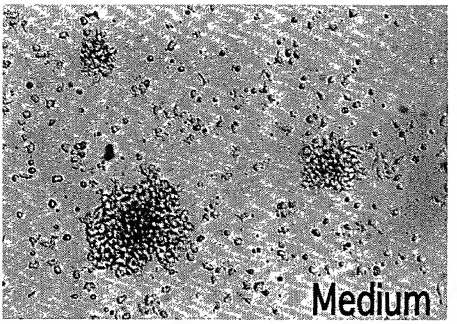


FIG. 6A

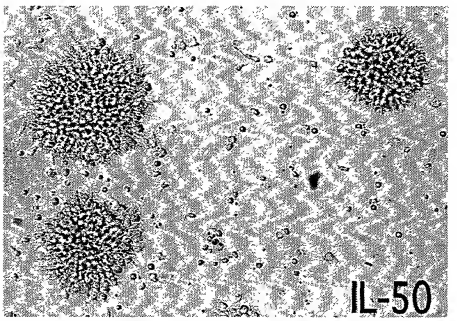


FIG. 6B

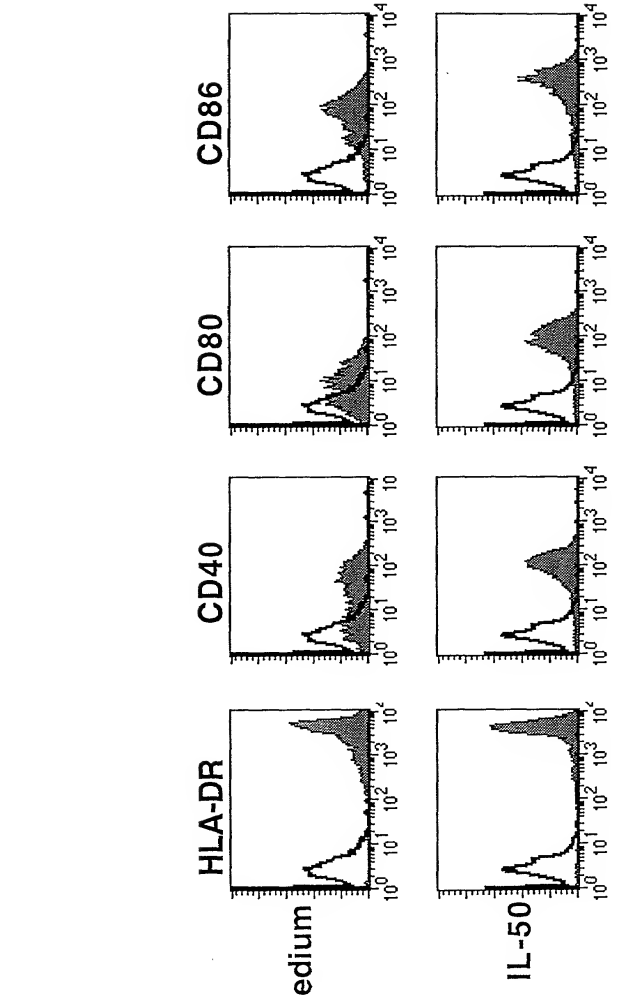


FIG. 7

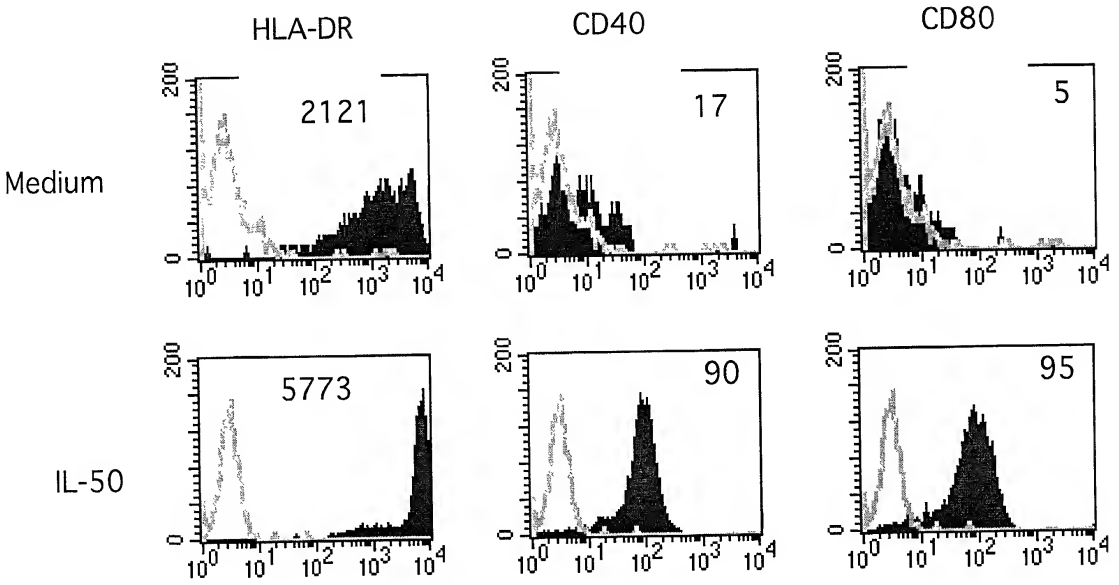

HLA-DR
CD40
CD80
Medium
IL-50
2121
17
5
5773
90
95
200
0
10^0 10^1 10^2 10^3 10^4

FIG. 8A

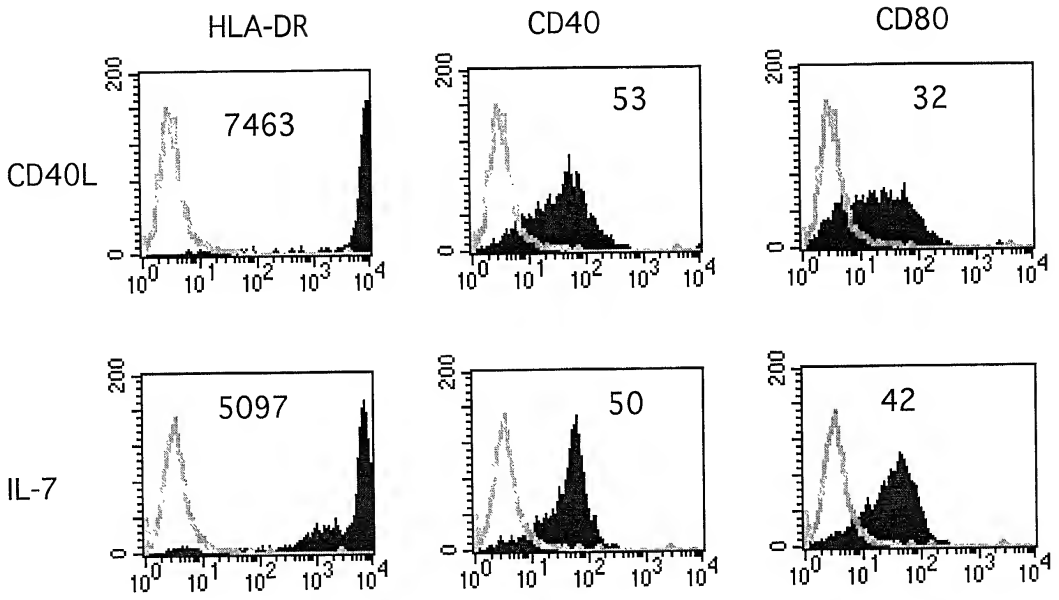

HLA-DR
CD40
CD80
CD40L
IL-7
7463
53
32
5097
50
42
200
0
10^0 10^1 10^2 10^3 10^4

FIG. 8B

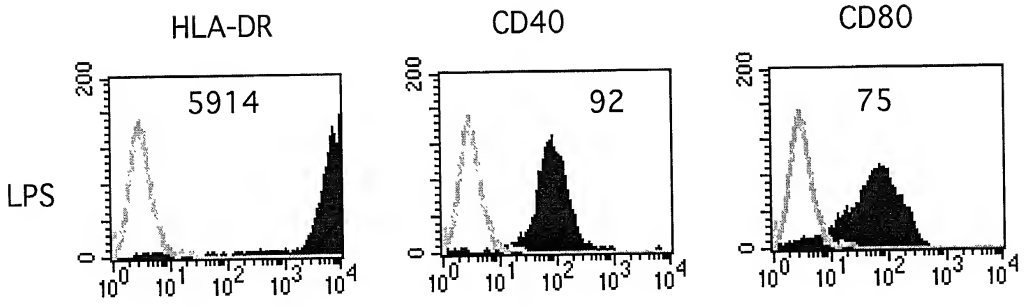


FIG. 8C

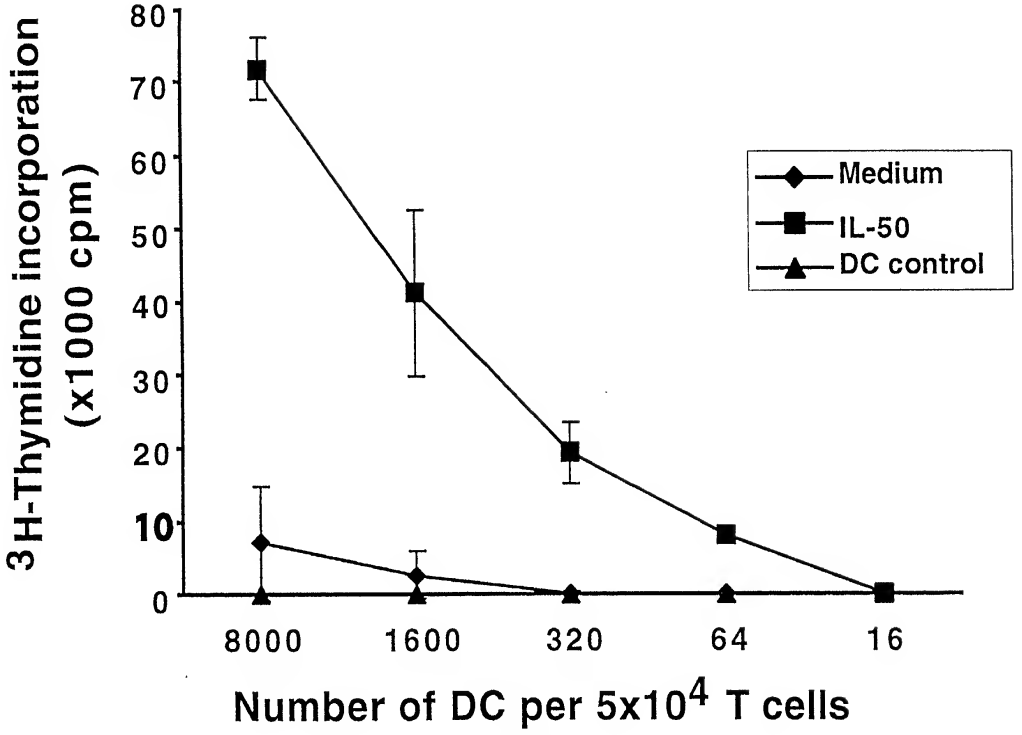

80
70
60
50
40
30
20
10
0
3H-Thymidine incorporation (x1000 cpm)
Medium
IL-50
DC control
8000
1600
320
64
16
Number of DC per 5x10^4 T cells

FIG. 9

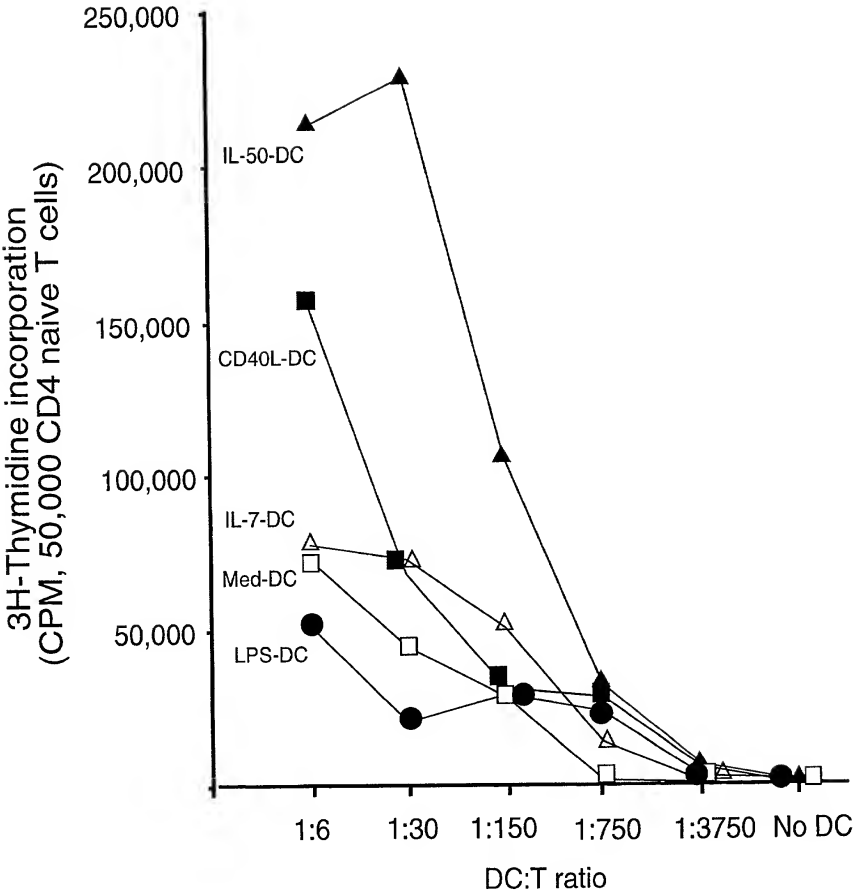

250,000
200,000
150,000
100,000
50,000
3H-Thymidine incorporation
(CPM, 50,000 CD4 naive T cells)
IL-50-DC
CD40L-DC
IL-7-DC
Med-DC
LPS-DC
1:6
1:30
1:150
1:750
1:3750
No DC
DC:T ratio

FIG. 10

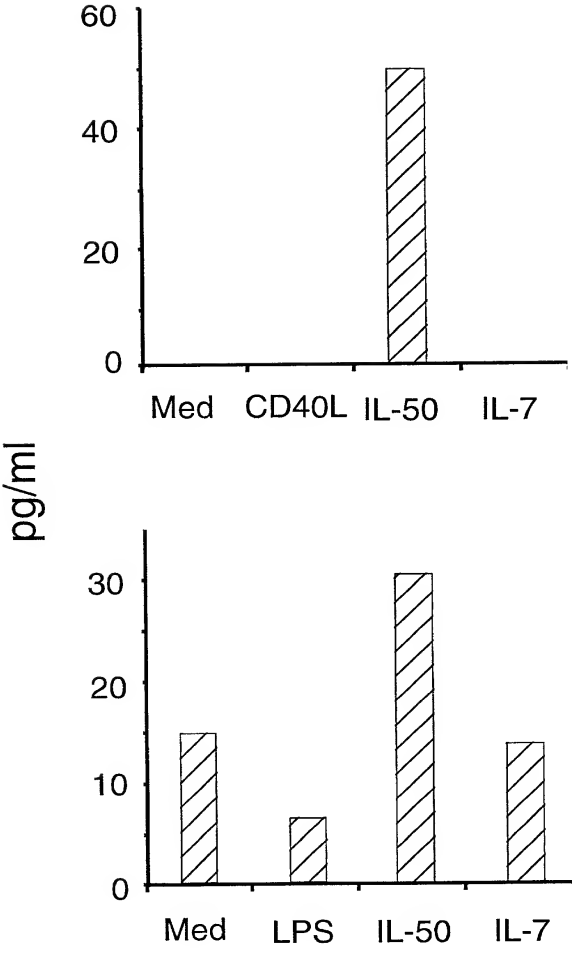


FIG. 11A

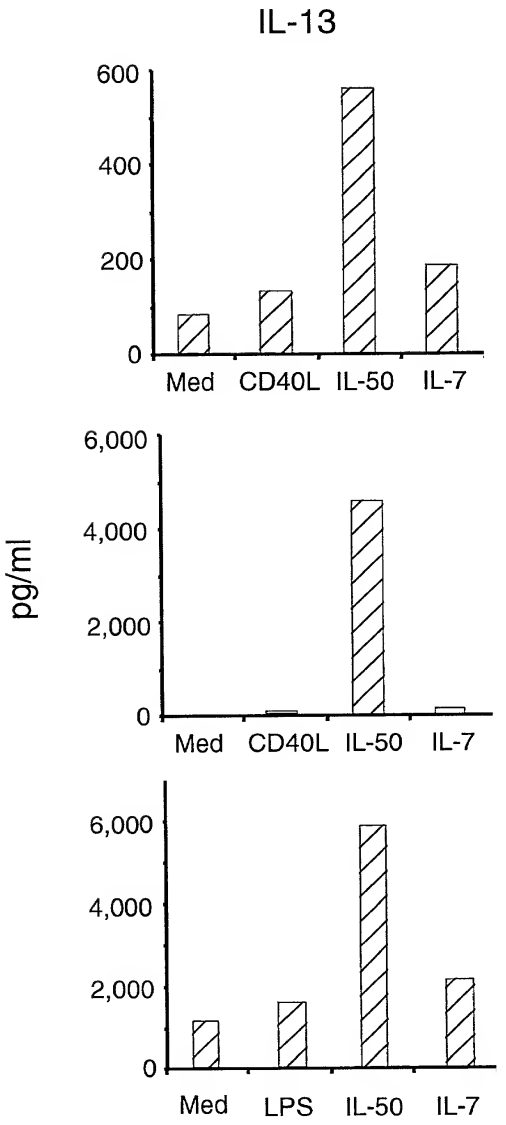

IL-13
600
400
200
0
Med
CD40L
IL-50
IL-7
pg/ml
6,000
4,000
2,000
0
Med
CD40L
IL-50
IL-7
6,000
4,000
2,000
0
Med
LPS
IL-50
IL-7

FIG. 11B

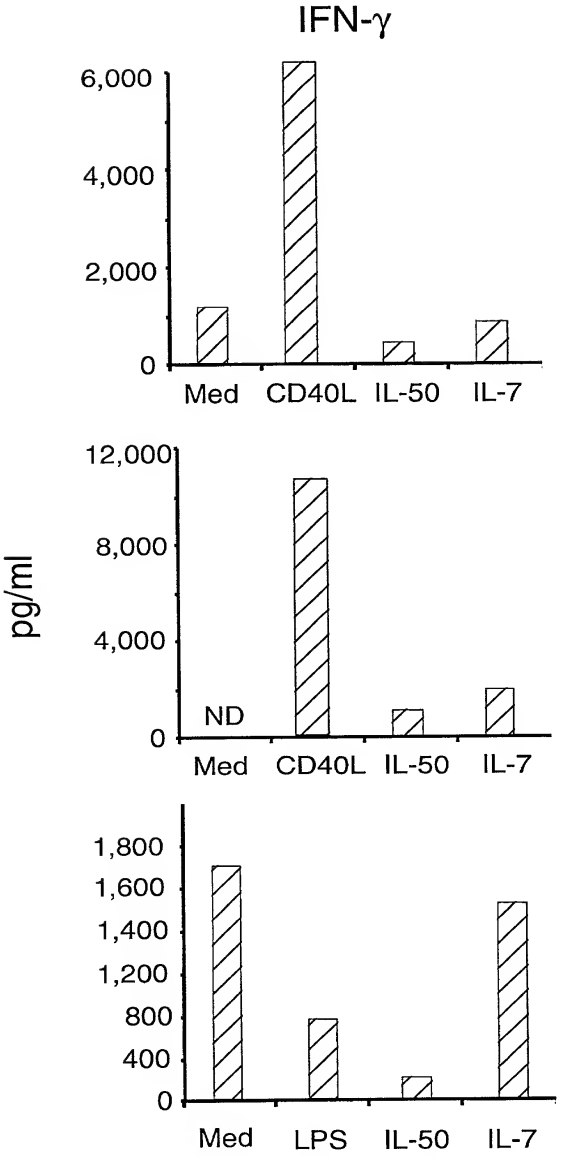

IFN-γ
6,000
4,000
2,000
0
Med
CD40L
IL-50
IL-7
pg/ml
12,000
8,000
4,000
ND
0
Med
CD40L
IL-50
IL-7
1,800
1,600
1,400
1,200
800
400
0
Med
LPS
IL-50
IL-7

FIG. 11C

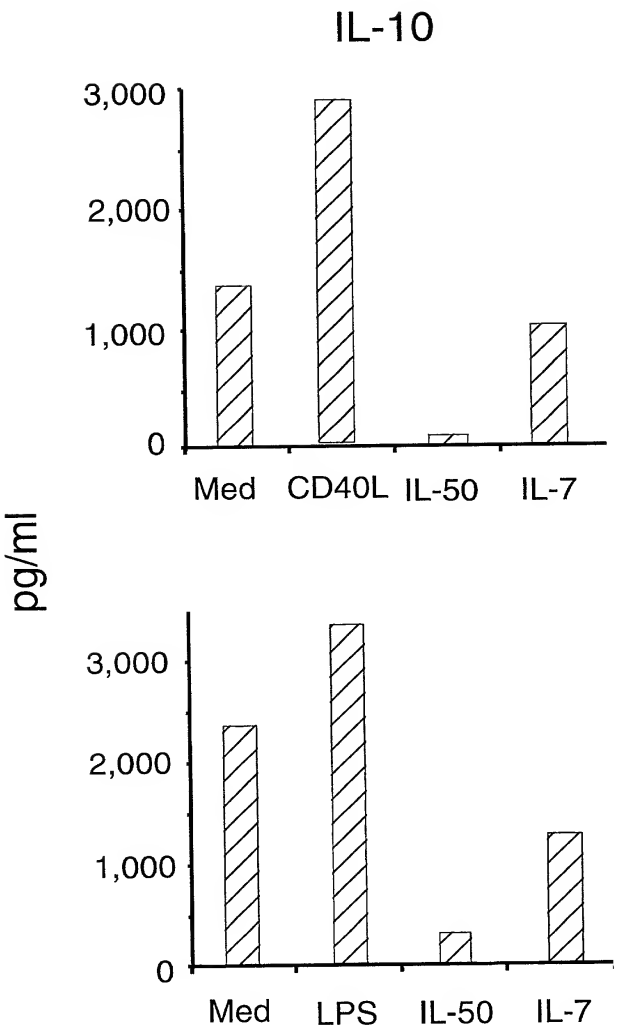

IL-10
3,000
2,000
1,000
0
Med
CD40L
IL-50
IL-7
pg/ml
3,000
2,000
1,000
0
Med
LPS
IL-50
IL-7

FIG. 11D

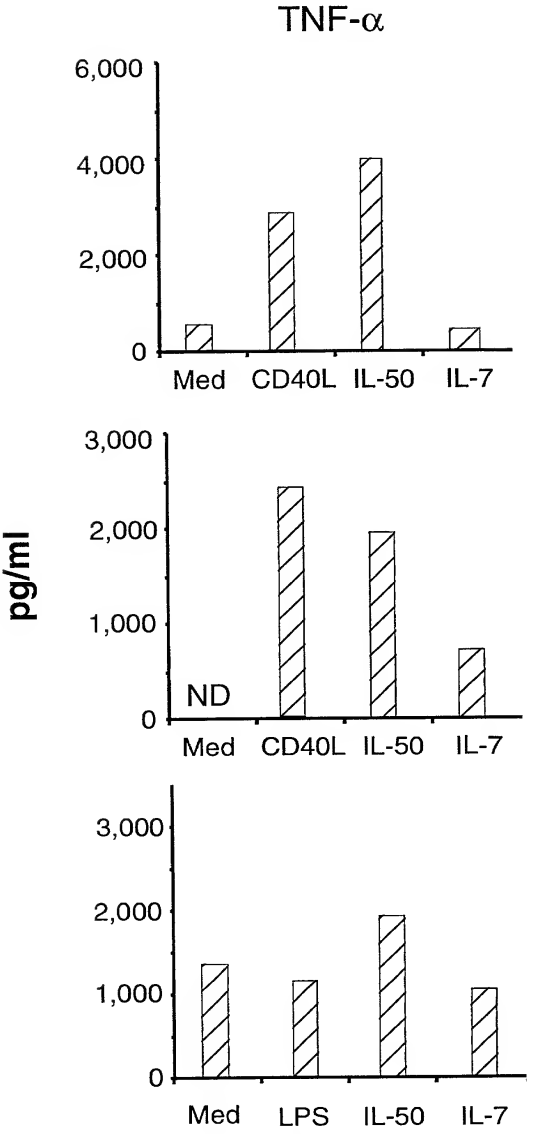

TNF-α
6,000
4,000
2,000
0
Med
CD40L
IL-50
IL-7
pg/ml
3,000
2,000
1,000
0
ND
Med
CD40L
IL-50
IL-7
3,000
2,000
1,000
0
Med
LPS
IL-50
IL-7

FIG. 11E

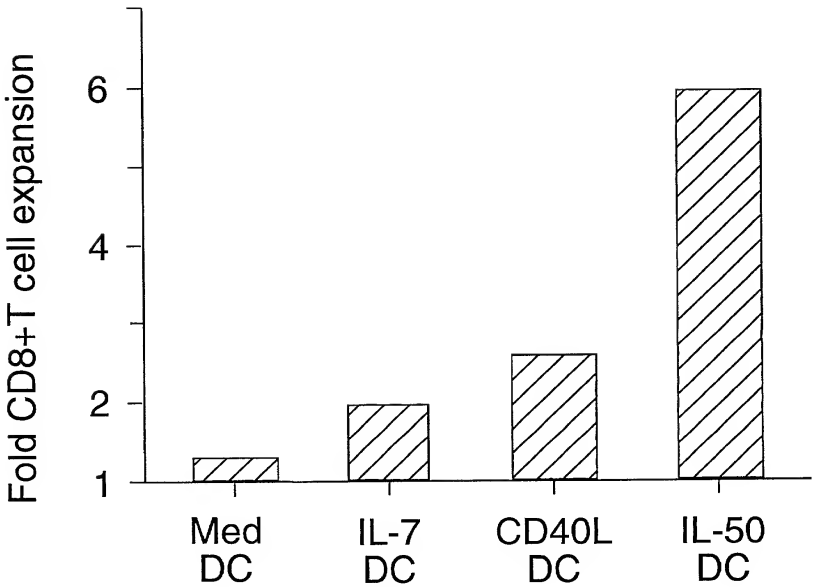


FIG. 12

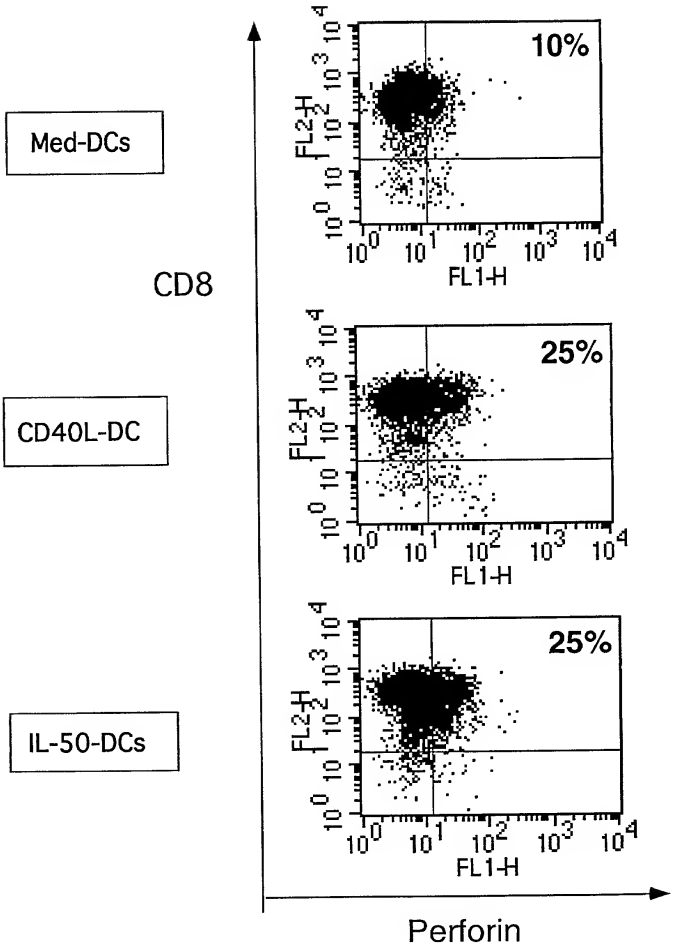


FIG. 13

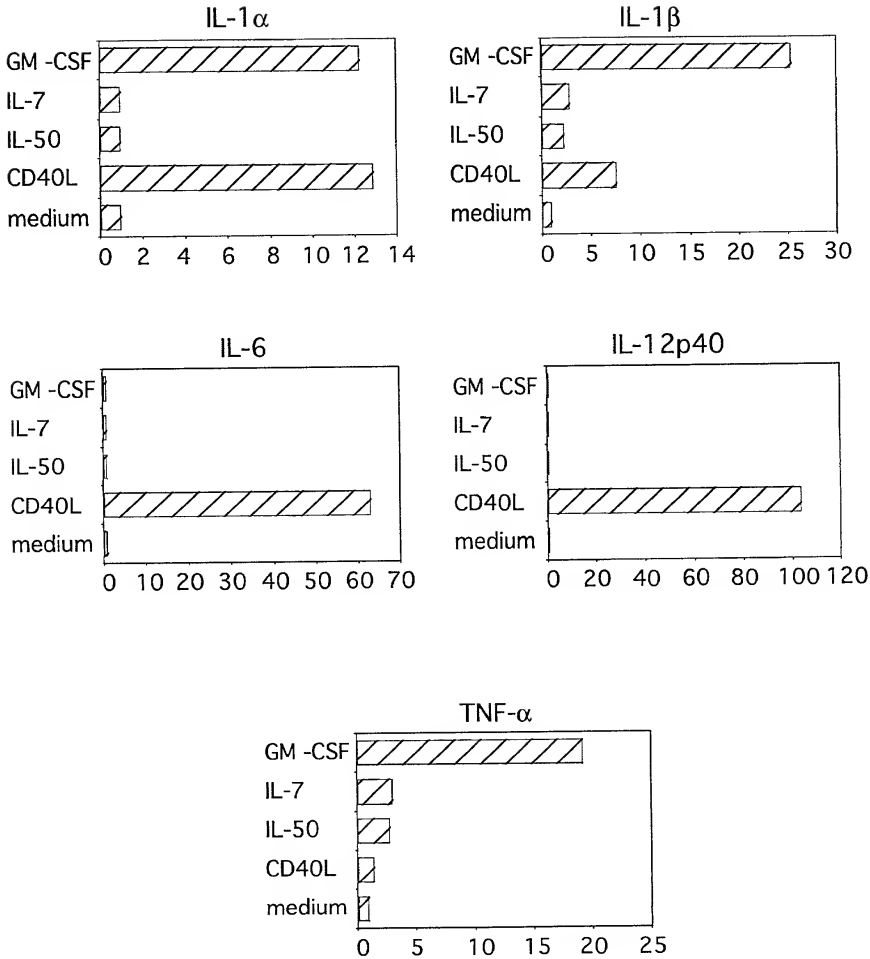
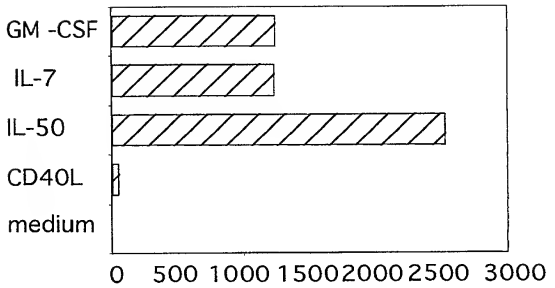

IL-1α
GM -CSF
IL-7
IL-50
CD40L
medium
0 2 4 6 8 10 12 14
IL-1β
GM -CSF
IL-7
IL-50
CD40L
medium
0 5 10 15 20 25 30
IL-6
GM -CSF
IL-7
IL-50
CD40L
medium
0 10 20 30 40 50 60 70
IL-12p40
GM -CSF
IL-7
IL-50
CD40L
medium
0 20 40 60 80 100 120
TNF-α
GM -CSF
IL-7
IL-50
CD40L
medium
0 5 10 15 20 25

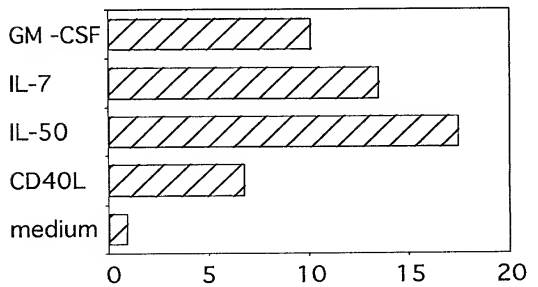
FIG.14A

Th2

TARC



MDC



DC+Naive

MIP3-beta

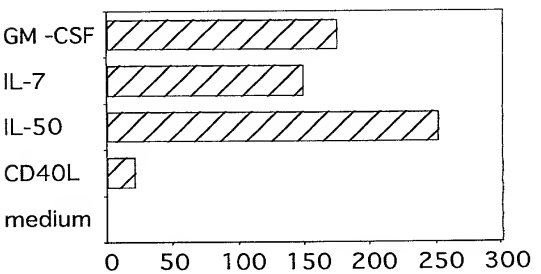


FIG. 14B

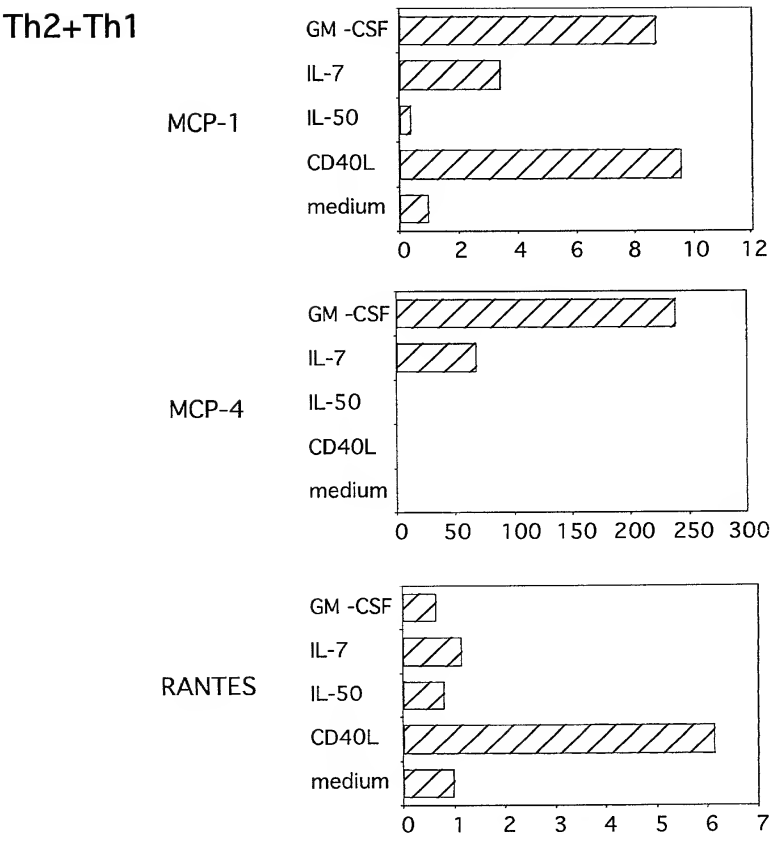

Th2+Th1
MCP-1
GM -CSF
IL-7
IL-50
CD40L
medium
0 2 4 6 8 10 12
MCP-4
GM -CSF
IL-7
IL-50
CD40L
medium
0 50 100 150 200 250 300
RANTES
GM -CSF
IL-7
IL-50
CD40L
medium
0 1 2 3 4 5 6 7
Th1
MIG
GM -CSF
IL-7
IL-50
CD40L
medium
0 10 20 30 40 50 60 70 80 90

FIG. 14C

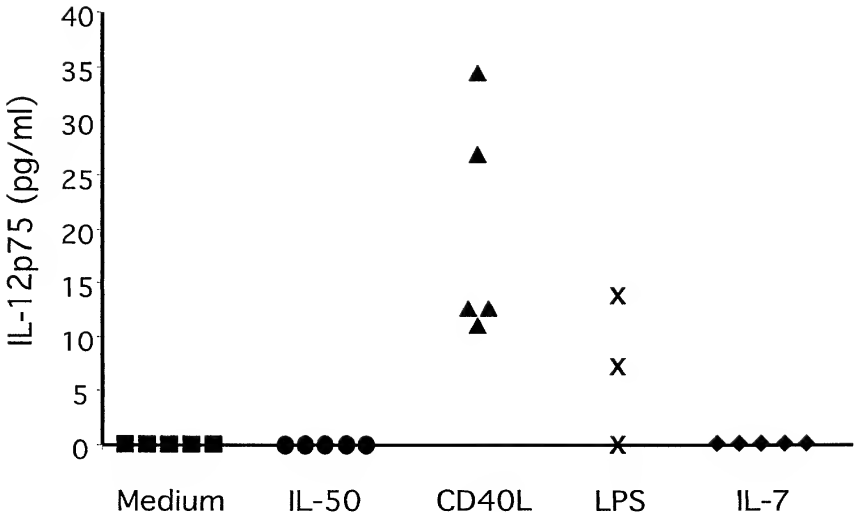


FIG. 15